IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s)	:	JAGER, et al.
Serial No.	:	09/451,739
Filed	:	November 30, 1999
For	:	ISOLATED NUCLEIC ACID MOLECULES ENCODING CANCER ASSOCIATED ANTIGENS, THE ANTIGENS PER SE, AND USES THEREOF
Group Art Unit	:	1642
Examiner	:	G. Nickol

December 8, 2000

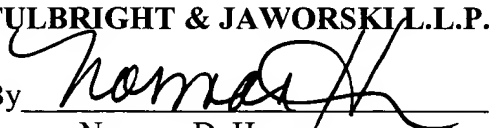Hon. Commissioner of Patents
  and Trademarks
Washington, D.C. 20231

LETTER RE
SEQUENCES

Responsive to the office action of December 1, 2000, a copy of which is attached, please replace the paper copy of sequence information in this case and the computer readable form thereof with the attached. The undersigned hereby declares that, to the best of his knowledge, the information on the submitted paper copy is identical to the information in the computer readable form of sequence information, and both are identical to information presented in the application as filed. No new matter is believed to be presented.

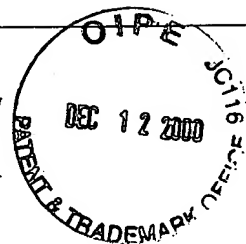Respectfully submitted,

FULBRIGHT & JAWORSKI L.L.P.

By

Norman D. Hanson
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703640.1

<110> Jager, Dirk
      Scanlan, Matthew
      Gure, Ali
      Jager, Elke
      Knuth, Alexander
      Old, Lloyd
      Chen, Yao-tseng

<120> Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigens,
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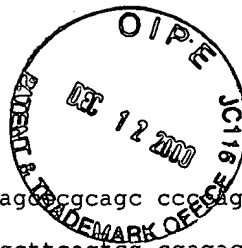<210> 1
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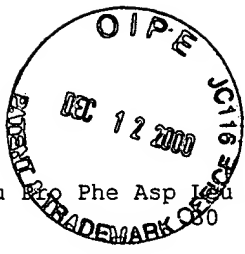
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        Ala Gln Lys Arg Arg Met Leu His Cys Val Gln Arg Ala Leu Ile Arg
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        Ser Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val
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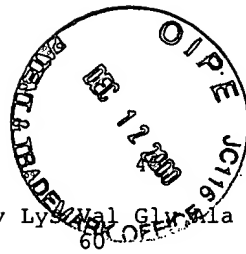
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Ser Gln Met Val Glu Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser
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His Val Glu Leu Phe Glu Ala Gln Gln Glu Leu Gly Asp Thr Val Gly
65                      70                      75                      80
Asn Ser Gly Lys Val Gly Ala Asp Arg Pro Asn Gly Asp Ala Val Ala
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Gln Ser Asp Lys Pro Asn Ser Lys Arg Ser Arg Arg Gln Arg Asn Asn
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Ser Gly Thr Pro Lys Glu Lys Lys Ala Lys Thr Ser Lys Lys Lys Lys
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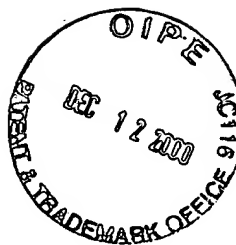<213> Homo sapiens
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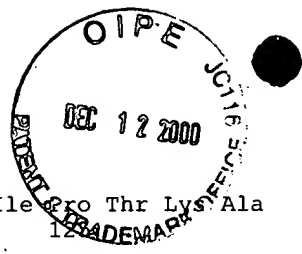
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Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln Met
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Arg Ala Arg Glu Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys
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Met Glu Gln Met Lys Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser
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Gly Arg Ile Glu Glu Gln His Arg Lys Glu Leu Glu Val Lys Gln Gln
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        340   345   350

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        355   360   365

Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu
370   375   380   385

Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr
                390   395   400

Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln Met
            405   410   415

Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr
        420   425   430

Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser
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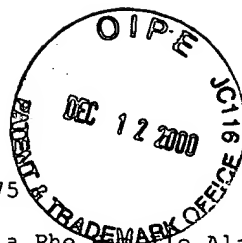
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Pro Arg Pro Ala Gly Pro Ala Arg Arg Gln Phe Gln Ala Ala Ser Leu
        35                  40                  45

Leu Thr Arg Gly Trp Gly Arg Ala Trp Pro Trp Lys Gln Ile Leu Lys
    50                  55                  60

Glu Leu Asp Glu Cys Tyr Glu Arg Phe Ser Arg Glu Thr Asp Gly Ala
65                  70                  75                  80

Gln Lys Arg Arg Met Leu His Cys Val Gln Arg Ala Leu Ile Arg Ser
                85                  90                  95

Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val Glu
            100                 105                 110

Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser His Val Glu Leu Phe
            115                 120                 125

Glu Ala Gln Gln Glu Leu Gly Asp Thr Val Gly Asn Ser Gly Lys Val
    130                 135                 140

Gly Ala Asp Arg Pro Asn Gly Asp Ala Val Ala Gln Ser Asp Lys Pro
145                 150                 155                 160

Asn Ser Lys Arg Ser Arg Arg Gln Arg Asn Asn Glu Asn Arg Glu Asn
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Ala Ser Ser Asn His Asp His Asp Asp Gly Ala Ser Gly Thr Pro Lys
            180                 185                 190

Glu Lys Lys Ala Lys Thr Ser Lys Lys Lys Lys Arg Ser Lys Ala Lys
```

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    210                215                220
Pro Thr Tyr Cys Leu Cys Asn Gln Val Ser Tyr Gly Glu Met Ile Gly
225                230                235                    240
Cys Asp Asn Asp Glu Cys Pro Ile Glu Trp Phe His Phe Ser Cys Val
            245                250                    255
Gly Leu Asn His Lys Pro Lys Gly Lys Trp Tyr Cys Pro Lys Cys Arg
            260                265                270
Gly Glu Asn Glu Lys Thr Met Asp Lys Ala Leu Glu Lys Ser Lys Lys
        275                280                285
Glu Arg Ala Tyr Asn Arg
    290                294
```

UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office
Address: COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
09/451,735	11/30/99	JAGER	LUD-5615

024972
FULBRIGHT & JAWORSKI, LLP
666 FIFTH AVE
NEW YORK NY 10103-3198

HM12/1201

NICKOL, G

EXAMINER
1642

ART UNIT	PAPER NUMBER
	9

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

PTO-90C (Rev. 2/95)

2 - Mail Copy

SERIAL NUMBER	FILING DATE		FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/451739				

RECEIVED

DEC 27 2000

TECH CENTER 1600/2900

EXAMINER	
ART UNIT	PAPER NUMBER

DATE MAILED:
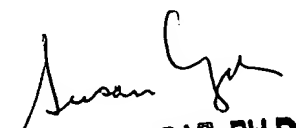
Please find below a communication from the EXAMINER in charge of this application

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures.

Any inquiry concerning this communication should be directed to Examiner **Gary Nickol, Ph.D.**, Art Unit **1642**, whose telephone number is **703-305-7143.**

Any inquiry of a general nature or relating to the status of this application should be directed to the Technology Center receptionist whose telephone number is (703) 308-0196.

APPLICANT IS GIVEN A <u>ONE MONTH</u> EXTENDABLE PERIOD WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Applicant is requested to return a copy of the attached Notice to Comply with the response.

SUSAN UNGAR, PH.D
PRIMARY EXAMINER

Application No.: 09/451739

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other: _____

Applicant Must Provide:

☒ An initial or <u>substitute</u> computer readable form (CRF) copy of the "Sequence Listing".

☒ An initial or <u>substitute</u> paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
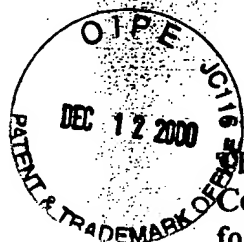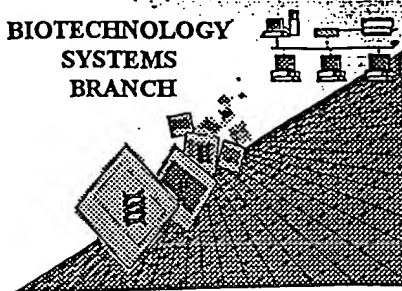PatentIn Software Program Support
     Technical Assistance..................................703-287-0200
     To Purchase PatentIn Software......................703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/451,739A

Source: 1642

Date Processed by STIC: 7/12/2000

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TECH CENTER 1600/2900

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JUL 28 2000

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

1642

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/451,739A   DATE: 07/12/2000
                                            TIME: 15:56:26

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Output Set: N:\CRF3\07122000\I451739A.raw

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 1 <110> APPLICANT: Jager, Dirk
 2           Scanlan, Matthew
 3           Gure, Ali
 4           Jager, Elke
 5           Knuth, Alexander
 6           Old, Lloyd
 7           Chen, Yao-tseng
 9 <120> TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigens,
10           the Antigens per se, and Uses Thereof
12 <130> FILE REFERENCE: LUD 5615
14 <140> CURRENT APPLICATION NUMBER: 09/451,739A
16 <141> CURRENT FILING DATE: 1999-11-30
18 <160> NUMBER OF SEQ ID NOS: 19
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ERRORED SEQUENCES

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530 <213> ORGANISM: Homo sapiens
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540         35                 40                 45
542 Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln
543     50                 55                 60
545 Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr
546 65                 70                 75                 80
548 Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys Glu
549                 85                 90                 95
551 Ile Asp Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asp Asn Asp Gly
552             100                105                110
554 Phe Leu Lys Ala Pro Cys Arg Met Lys Val Ser Ile Pro Thr Lys Ala
555         115                120                125
557 Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys
558     130                135                140
560 Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn
561 145                150                155                160
563 Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln Met
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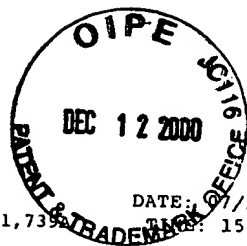
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PATENT APPLICATION:   US/09/451,739   DATE: 07/12/2000
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      572 Lys Ala Thr His Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu
      573         210              215              220
      575 Asp Ser Thr Ser Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu
      576 225              230              235              240
      578 Arg Ala Arg Glu Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys
E--> 579         260 245              265 250              270 255
      581 Met Glu Gln Met Lys Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser
E--> 582     275 260              280 265              285 270
      584 Glu Ala Lys Glu Ile Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp
E--> 585     290 271              295 280          300 285
      587 Glu Gln Glu Leu Cys Ser Val Arg Leu Thr Leu Asn Gln Glu Glu Glu
E--> 588 305              310              315              320
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E--> 591              325              330              335
      593 Gly Arg Ile Glu Glu Gln His Arg Lys Glu Leu Glu Val Lys Gln Gln
E--> 594              340              345              350
      596 Leu Glu Gln Ala Leu Arg Ile Gln Asp Ile Glu Leu Lys Ser Val Glu
E--> 597     355              360              365
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E--> 600     370              375              380
      602 Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu
E--> 603 385              390              395              400
      605 Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr
E--> 606              405              410              415
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E--> 609              420              425              430
      611 Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr
E--> 612     435              440              445
      614 Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser
E--> 615     450              455              460
      617 Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu
E--> 618 465              470              475              480
      620 Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile
E--> 621              485              490              495
      623 Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp
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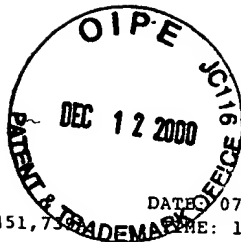
numbers off

FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/451,7~~~~~~~~~ DATE: 07/12/2000
~~~~~~~~~~~~~~ TIME: 15:56:27
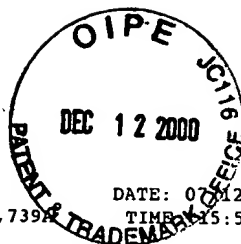
Input Set : A:\lud-5615.txt
Output Set: N:\CRF3\07122000\I451739A.raw

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L:28  M:283 W: Missing Blank Line separator, <400> field identifier
L:35  M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:35  M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:86  M:283 W: Missing Blank Line separator, <220> field identifier
L:87  M:283 W: Missing Blank Line separator, <400> field identifier
L:133 M:283 W: Missing Blank Line separator, <220> field identifier
L:134 M:283 W: Missing Blank Line separator, <400> field identifier
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L:167 M:283 W: Missing Blank Line separator, <400> field identifier
L:203 M:283 W: Missing Blank Line separator, <220> field identifier
L:204 M:283 W: Missing Blank Line separator, <400> field identifier
L:264 M:283 W: Missing Blank Line separator, <220> field identifier
L:265 M:283 W: Missing Blank Line separator, <400> field identifier
L:313 M:283 W: Missing Blank Line separator, <220> field identifier
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L:365 M:283 W: Missing Blank Line separator, <220> field identifier
L:368 M:283 W: Missing Blank Line separator, <400> field identifier
L:391 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:391 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
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L:437 M:283 W: Missing Blank Line separator, <400> field identifier
L:445 M:283 W: Missing Blank Line separator, <220> field identifier
L:446 M:283 W: Missing Blank Line separator, <400> field identifier
L:454 M:283 W: Missing Blank Line separator, <220> field identifier
L:457 M:283 W: Missing Blank Line separator, <400> field identifier
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L:520 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
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L:531 M:283 W: Missing Blank Line separator, <220> field identifier
L:532 M:283 W: Missing Blank Line separator, <400> field identifier
L:579 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:582 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
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JUL 28 2000

TECH CENTER 1600/2900

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/451,739   DATE: 07/12/2000
TIME: 15:56:27

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Output Set: N:\CRF3\07122000\I451739A.raw

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L:594 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:597 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:600 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:603 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:606 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:609 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:612 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:615 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:618 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:621 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:624 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:627 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:627 M:252 E: No. of Seq. differs, <211>LENGTH:Input:528 Found:512 SEQ:16
L:634 M:283 W: Missing Blank Line separator, <220> field identifier
L:635 M:283 W: Missing Blank Line separator, <400> field identifier
L:643 M:283 W: Missing Blank Line separator, <220> field identifier
L:644 M:283 W: Missing Blank Line separator, <400> field identifier
L:652 M:283 W: Missing Blank Line separator, <220> field identifier
L:653 M:283 W: Missing Blank Line separator, <400> field identifier
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